



09/589285

Neutrokin- α

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC 60

61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC 120

121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180
1 M D D S T E R E Q S R L 12

181 TTA CT TCT TGCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGTTTCCATCCTCC 240
13 T S C L K K R E E M K L K E C V S I L P 32
CD-I

241 CACGGAAGGAAAGCCCCTCTGTCCGATCCTCAAAGACGGAAAGCTGCTGGCTGCAACCT 300
33 R K E S P S V R S S K D G K L L A A T L 52
CD-I

301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCC 360
53 L L A L L S C C L T V V S F Y Q V A A L 72

361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC 420
73 Q G D L A S L R A E L Q G H H A E K L P 92
CD-II

421 CAGCAGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTACCGCGGGAC 480
93 A G A G A P K A G L E E A P A V T A G L 112
CD-III

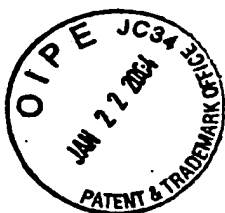
481 TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540
113 K I F E P P A P G E G N S S Q N S R N K 132

541 AGCGTGCCGTTCAAGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG 600
133 R A V Q G P E E T V T Q D C L Q L I A D 152
CD-IV

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FIG. 1A

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Neutrokin- α

601 ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT 660
153 S E T P T I Q K G S Y T F V P W L L S F 172
CD-V

661 TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTT 720
173 K R G S A L E E K E N K I L V K E T G Y 192
CD-V CD-VI

721 ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA 780
193 F F I Y G Q V L Y T D K T Y A M G H L I 212
CD-VI CD-VII

781 TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT 840
213 Q R K K V H V F G D E L S L V T L F R C 232
CD-VII CD-VIII

841 GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAA 900
233 I Q N M P E T L P N N S C Y S A G I A K 252
CD-VIII CD-IX

901 AACTGGAAGAAGGAGATGAACTCCAACCTTGCAATACCAAGAGAAAATGCACAAATATCAC 960
253 L E E G D E L Q L A I P R E N A Q I S L 272
CD-X

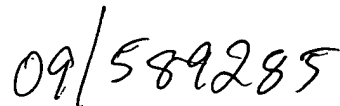
961 TGGATGGAGATGTCACATTTTTTGGTGCAATTGAACTGCTGTGACCTACTTACACCATGT 1020
273 D G D V T F F G A L K L L 285
CD-XI

1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA 1080

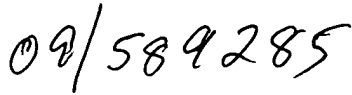
1081 CCAAAAAAAAAAAAAAAAAA 1100

FIG.1B

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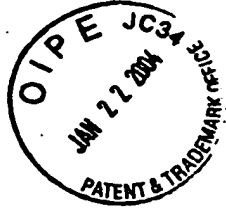
	10	20	30	
1	MSTESMIRDVEL	- - - - -	- - - AEEA	TNFalpha
1	- - - - -	- - - - -	- - - TPERL	TNFbeta
1	GA - - - - -	- - - - -	- - - - -	LTbeta
1	QQPFNYPPIYW	VDSSASSPW	APP GTV	FasLigand
1	MDDSTEREQSRL	TSCCLKKREEMKL	KECVSI	Neutrokine alpha
1	MDDSTEREQSRL	TSCCLKKREEMKL	KECVSI	Neutrokine alphaSV
	40	50	60	
17	LPKKTGGPQ	- GSRR	- - - - -	TNFalpha
8	F - - - - -	- - - - -	- - - - -	TNFbeta
4	- - - LGLEGRGG	- - - - -	- - - - -	LTbeta
30	LPCTSVPRRP	QRRPPPPPPPP	LP PPPP	FasLigand
31	LPRKESPSVRS	SKD - - - GKLLAAT	LL LALL	Neutrokine alpha
31	LPRKESPSVRS	SKD - - - GKLLAAT	LL LALL	Neutrokine alphaSV
	70	80	90	
30	- - - - -	- - - - -	- C L F L S L F S	TNFalpha
9	- - - - -	- - - - -	- - - L L L V L L P	TNFbeta
12	- - - - -	- - - - -	- - - L L V A G A T S L V T	LTbeta
60	PPPLPPLP	PP L K K R G N H S T G L C L L V M F F M	- - - - -	FasLigand
58	SCCLTVVSF	YQVAAAL	QGD L A S L R A E L Q G H H	Neutrokine alpha
58	SCCLTVVSF	YQVAAAL	QGD L A S L R A E L Q G H H	Neutrokine alphaSV



	100	110	120	
38	F L - - I V A G A T T L F C L L H F G V I G P Q R E E F P R			TNFalpha
31	G A Q G L P G V G L - - - - - - - - - - - - - - -			TNFbeta
32	L L L A V P I T V L A V L A L V P Q D Q G G L V T E T A D P			LTbeta
90	V L V A L V G L G L G M F Q L F H L Q K E L A E L R E S T S			FasLigand
88	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alpha
88	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alphaSV

	130	140	150	
66	D L S L I S - P L A - Q A V R S S S R T P S D - - - K P V A			TNFalpha
41	- - - T P S - A A Q - T A R Q H P K M H L A H S T L K P A A			TNFbeta
62	G A Q A Q Q - G L G F Q K L P E E E P E T D L S P G L P A A			LTbeta
120	Q M H T A S - S L E - K Q I G H P S P P P E K K E L R K V A			FasLigand
118	P A P G E G N S S Q N S R N K R A V Q G P E E T V T Q D C L			Neutrokin alpha
118	P A P G E G N S S Q N S R N K R A V Q G P E E T - - - - -			Neutrokin alphaSV

	160	170	180	
91	H V V A N P Q A E G - Q - - - - - L Q W L N R R A N A L L			TNFalpha
66	H L I G D P S K Q N - S - - - - - L W R A N T D R A F L			TNFbeta
91	H L I G A P L K - G Q G - - - - - L G W E T T K E Q A F L			LTbeta
148	H L T G K S N S R S M P - - - - - L E W E D T Y G I V L L			FasLigand
148	Q L I A D S E T P T I Q K G S Y T F V P W L - - - L S F K			Neutrokin alpha
142	- - - - - - - - - - - G S Y T F V P W L - - - L S F K			Neutrokin alphaSV



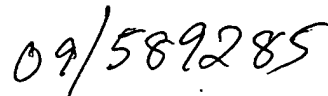
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	190	200	210	
114	A N G V E L R D N - Q L V V P P S E G L Y L I Y S Q V L F K G			TNFalpha
89	Q D G F S L S N N - S L L V P P T S G I Y F V Y S Q V V F S G			TNFbeta
114	T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L V G Y R G G			LTbeta
172	- S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G G			FasLigand
174	R G S A L E E K E N K I L V K E E T G Y F F I Y G Q V L Y T D			Neutrokine alpha
155	R G S A L E E K E N K I L V K E E T G Y F F I Y G Q V L Y T D			Neutrokine alphaSV

	220	230	240	
143	Q G C P - - - - S T H V L L T H T I S R I A V S Y Q T K			TNFalpha
118	K A Y S P - - K A T S S P L Y L A H E V Q L F S S Q Y P F H			TNFbeta
144	R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G G			LTbeta
200	Q S C N - - - - N L P L S H K V Y M R N S K Y P Q D			FasLigand
204	K T Y A M G - - - - H L I Q R K K K V H V F G D E L S - -			Neutrokine alpha
185	K T Y A M G - - - - H L I Q R K K K V H V F G D E L S - -			Neutrokine alphaSV

	250	260	270	
167	V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E			TNFalpha
146	V P - - L L S S Q K M V Y P - - - - G L Q E P W L H			TNFbeta
174	T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T			LTbeta
222	L V - - M M E G K M M S Y C - - - - T T G Q M W A R			FasLigand
226	L V T L F R C I Q N M P E T L P N - - - - - N			Neutrokine alpha
207	L V T L F R C I Q N M P E T L P N - - - - - N			Neutrokine alphaSV

FIG.2C



		280		290		300	
193	P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E						TNFalpha
166	S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P						TNFbeta
204	S V G F G G L V Q L R R G G E R V Y V N I S H P D M V D F A R						LTbeta
242	S S Y L G A V F N L T S A D H L T V N V S E L S L V N F F E E						FasLigand
244	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D						Neutrokin alpha
225	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D						Neutrokin alphaSV

		310	
223	S G Q V Y F G I I A L		TNFalpha
196	S - T V F F G A F A L		TNFbeta
234	- G K T F F G A V M V G		LTbeta
272	S - Q T F F G L Y K L		FasLigand
274	G D V T F F G A L K L L		Neutrokin alpha
255	G D V T F F G A L K L L		Neutrokin alphaSV

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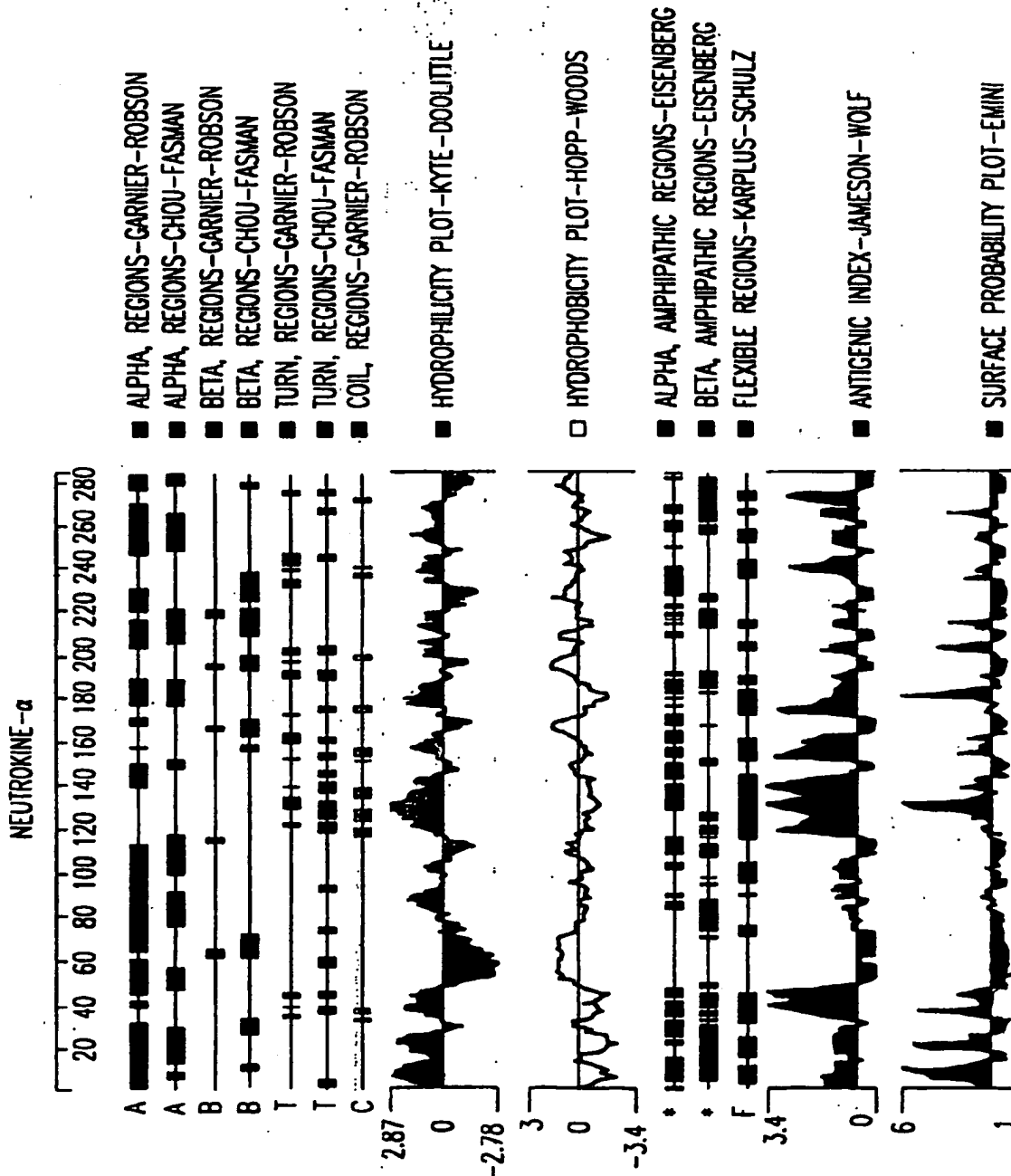


FIG.3



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	1				50
HSOAD55RA	GGNTAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HNEDU15X	...AAATTCA	GGATAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HSLAH84R	.AATTCGGCA	NAGNAACTG	GTTACTTTTT	TATATATGGT	CAGGTTTTAT
HLTBM08R	AATTCGGCAC	GAGCAAGGCC	GGCCTGGAGG	AAGCTCCAGC	TGTCACCGCG
	51				100
HSOAD55R	GTGCACGCAG	GACATCANCA	A..ACACANN	NNNCAGGAAA	TAATCCATTG
HNEDU15X	GTGCACGCAG	GACATCAACA	A..ACACAGA	TAACAGGAAA	TGATCCATTG
HSLAH84R	ATACTGATAA	GACCTACGCC	ATGGGACATC	TAGTTCAGAG	GAAGAAGGTC
HLTBM08R	GGACTGAAAA	TCTTTGAACC	ACCAGCTCCA	GGAGAAGGCA	ACTCCAGTCA
	101				150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA	AGGCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HNEDU15X	CCTGTGGTCA	CTTATTCTAA	AGGCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HSLAH84R	CATGTCTTTG	GGGATGAATT	GAGTCTGGTG	ACTTTGTTTC	GATGTATTCA
HLTBM08R	GAACAGCAGA	AATAAGCGTG	CCGTTCAGGG	TCCAGAAGAA	ACAGTCACTC
	151				200
HSOAD55R	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HNEDU15X	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HSLAH84R	AAATATGCCT	GAAACACTAC	CCAATAATTC	CTGCTATTCA	GCTGGCATTG
HLTBM08R	AAGACTGCTT	GCAACTGNNT	GCAGACAGTG	AAACACCAAC	TATACAAAAA
	201				250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA	CTGNAAGGAG	TGTGTTTCCA	TCCTCCCACG
HNEDU15X	AGAAAAGAGA	AGAAATGAAA	CT.GAAGGAG	TGTGTTTCCA	TCCTCCCACG
HSLAH84R	CAAACTGGN	AGGAAGGA..	...GATGAAC	TCCAACCTGC	AATACCAGGG
HLTBM08R	GGCTCCCTTC	TGNTGCCACA	TTTGGGCCAA	GGAATGGAGA	GATTTCTTCG
	251				300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HSLAH84R	GAAAATGCAC	AATTATCACT	GGGATGGAGA	TGTTACATT	TTTTGGGTGC
HLTBM08R	TCTGGAAACA	TTTTGCCAAA	CTCTTCAGAT	ACTCTTTNCT	CTCTGGGAAT
	301				350
HSOAD55R	CAACCTTGNT	GNTGGCATTG	TGTTCTTGCT	GNCTCAAGGT	GGTGTNTT.
HNEDU15X	CAACCTTGCT	GCTGGCACTG	CTGTCTTGCT	GCCTCACGGT	GGTGTCTTTC
HSLAH84R	CATTGAAACT	GCTGTGACCT	NCTTACANCA	NGTGCTGTTN	GCTATTTTNC
HLTBM08R	CAAAGGAAAA	TCTCTACTTA	GATTNACACA	TTTGTTCCTA	TGGGTNTCTT
	351				400
HSOAD55R
HNEDU15X	TACCAGGTGG	CCGCCCTGCA	AGGGGACCTG	GCCAGCCTCC	GGGCAGAGCT
HSLAH84R	CTNCCTNTTG	TNTGGTAACC	TCTTAGGAAG	GAAGGATTCT	TAAGTGGGAA
HLTBM08R	AAGTTTTAAA	AGGGGAGTGC	CCTTAGGAGG	AAAAGGGGAT	AAATATTGGC

FIG.4A



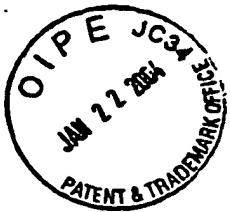
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	401		450
HSOAD55R
HNEDU15X	GCAGGGCCAC	CACGCGGAGA	AGCTGCCAGC
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC
		AGGAGCAGGA	GCCCCCAAGG
		GNNANANGNG	GGGNGTTNN
		AGGTTTNTAT	ANCTGGTAGG
	451		500
HSOAD55R
HNEDU15X	CCGGCCTGGA	GGAAGCTCCA	GCTGTCACCG
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG
		NCNNTCTTTT	GGGNTGA...
	501		550
HSOAD55R
HNEDU15X	CCACCAGCTC	GAGGAGAAGG	CAACTCCAGT
HSLAH84R	CNANGGGGGN	TTTTT.....
HLTBM08R
	551		600
HSOAD55R
HNEDU15X	TGCCGTTCAG	GGTCCAGAAG	AAACAGTCAC
HSLAH84R
HLTBM08R
	601		650
HSOAD55R
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA
HSLAH84R
HLTBM08R
	651		700
HSOAD55R
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT
HSLAH84R
HLTBM08R
	701		750
HSOAD55R
HNEDU15X	TAAAATATTG	GTCAAAGAAA	CTGGTTACTT
HSLAH84R
HLTBM08R
	751		800
HSOAD55R
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC
HSLAH84R
HLTBM08R

FIG.4B

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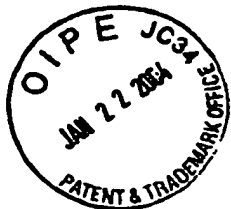
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	801		850
HSOAD55R
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R
HLTBM08R
	851		900
HSOAD55R
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R
HLTBM08R
	901		950
HSOAD55R
HNEDU15X	TTGCAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R
HLTBM08R
	951		1000
HSOAD55R
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R
HLTBM08R
	1001		1050
HSOAD55R
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R
HLTBM08R
	1051		1100
HSOAD55R
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R
HLTBM08R
	1101		
HSOAD55R		
HNEDU15X	AAAAAA		
HSLAH84R		
HLTBM08R		

FIG.4C

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Neutrokin- α SV

1 ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA 60
1 M D D S T E R E Q S R L T S C L K K R E 20

61 GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCCTCTGTCCGA 120
21 E M K L K E C V S I L P R K E S P S V R 40
CD-I

121 TCCTCAAAGACGGAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC 180
41 S S K D G K L L A A T L L L A L L S C C 60
CD-I

181 CTCACGGTGGTGTCTTTCTACAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG 240
61 L T V V S F Y Q V A A L Q G D L A S L R 80
CD-II

241 GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCC 300
81 A E L Q G H H A E K L P A G A G A P K A 100
CD-II CD-III

301 GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA 360
101 G L E E A P A V T A G L K I F E P P A P 120
CD-III

#

361 GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTTCAGGGTCCAGAAGAA 420
121 G E G N S S Q N S R N K R A V Q G P E E 140

421 ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA 480
141 T G S Y T F V P W L L S F K R G S A L E 160
CD-IV

481 GAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTATATATGGTCAGGTT 540
161 E K E N K I L V K E T G Y F F I Y G Q V 180
CD-IV CD-V

541 TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC 600
181 L Y T D K T Y A M G H L I Q R K K V H V 200
CD-VI CD-VII

FIG.5A

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Neutrokin- α SV

601 TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA 660
201 F G D E L S L V T L F R C I O N M P E T 220
CD-VIII CD-VIII

661 CTACCCAATAATTCCTGCTATTGAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTC 720
221 L P N N S C Y S A G I A K L E E G D E L 240
CD-IX CD-X

721 CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT 780
241 Q L A I P R E N A Q I S L D G D V T F F 260
CD-X CD-XI

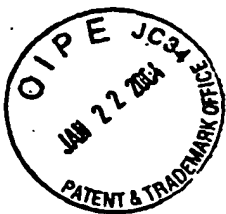
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261 G A L K L L 266
CD-XI

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900

901 AAA 903

FIG.5B

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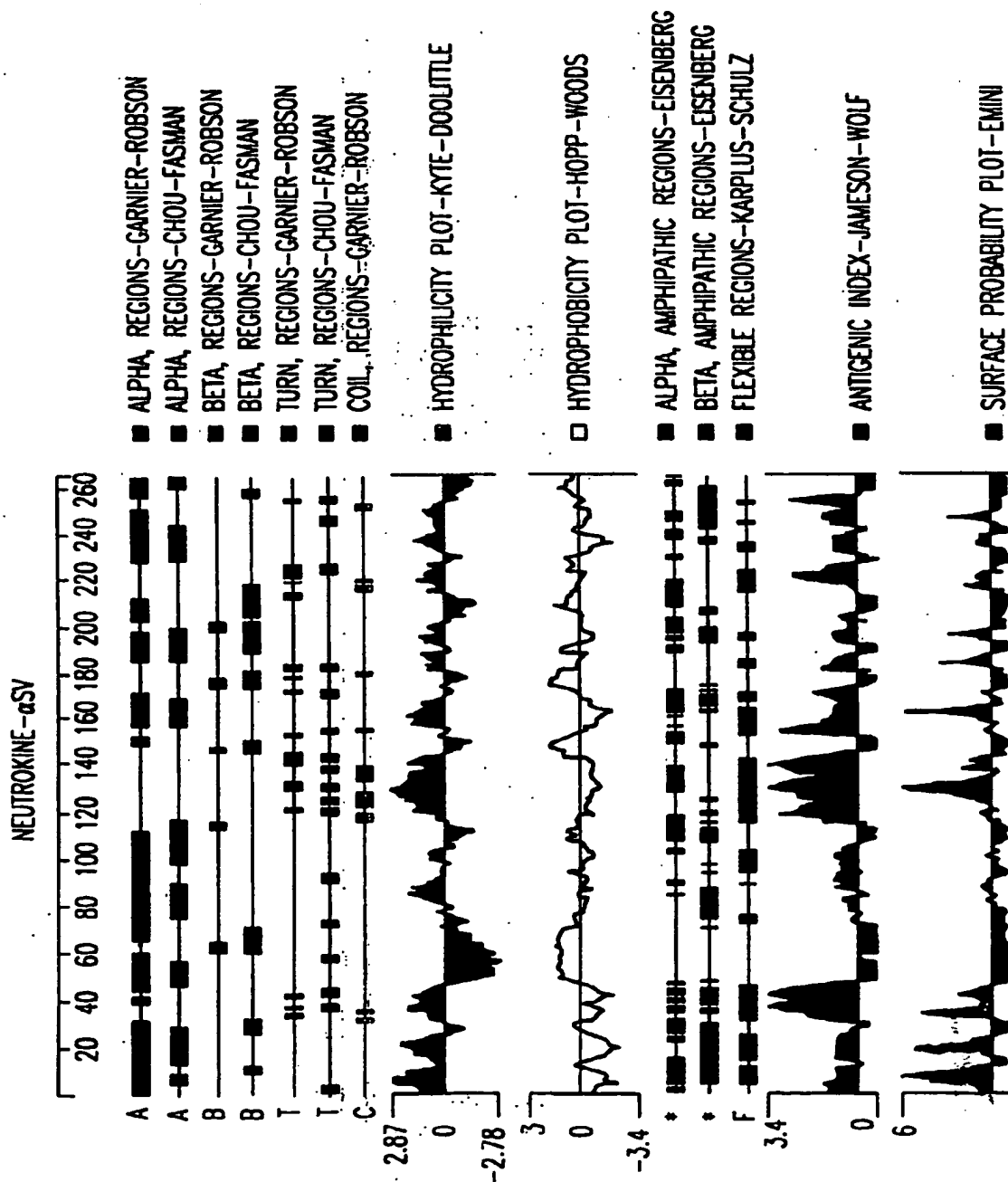


FIG.6

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